

Lake name and location	Environment details	Techniques used	Organisms identified	Key metabolisms/ processes	Notes	Reference	Figure 1 map location
Lakes Bonney, Hoare, Fryxell, Joyce, Miers and Vanda, McMurdo Dry Valleys	Fresh to hypersaline, permanently ice-covered	16S and <i>amoA</i> libraries	β -proteobacteria & γ -proteobacteria	Ammonia oxidation	Nitrifying bacterial <i>amoA</i> detected in all lakes. In meromictic lakes, the population of β - and γ -proteobacteria vertically stratified. Majority of nitrifying bacteria were β -proteobacteria.	Voytek <i>et al.</i> , 1999	McMurdo Sound, Victoria Land & Transantarctic Mountains
Lake Bonney, McMurdo Dry Valleys	Hypersaline, meromictic, permanently ice-covered, lake separated into east and west lobes	<i>nifH</i> library of ice aggregate material and microbial mats nitrogenase activity assays	Cyanobacteria, γ -proteobacteria. α -proteobacteria & δ -proteobacteria	Nitrogen fixation by both cyanobacteria and heterotrophic bacteria	Nitrogenase activity low compared to temperate environments. Heterotrophs responsible for 10–30% of nitrogenase activity. Heterotrophs likely microaerophilic.	Olson <i>et al.</i> , 1998	McMurdo Sound, Victoria Land & Transantarctic Mountains
Lake Bonney, McMurdo Dry Valleys & Terrestrial cyanobacterial mats from Taylor Valley	Hypersaline, meromictic, permanently ice-covered, lake separated into east and west lobes	16S library of sediment trapped in ice and hybridization of probes against surrounding mats	Cyanobacteria, Acidobacterium/Holophaga, Planctomycetales & Green non-sulfur Bacteria	Phototrophy and heterotrophy	Probes designed from 16S clone library of bacteria in the sediment in the ice matched that of the surrounding mats.	Gordon <i>et al.</i> , 2000	McMurdo Sound, Victoria Land & Transantarctic Mountains
Lake Bonney, McMurdo Dry Valleys	Hypersaline, meromictic, permanently ice-	16S libraries of deep	γ -proteobacteria, Actinobacteria, CFB, Firmicutes, α -proteobacteria, β -	Heterotrophy	Population vertically stratified. East and West Lobes have overlapping but	Glatz <i>et al.</i> , 2006	McMurdo Sound, Victoria Land &

	covered, lake separated into east and west lobes	waters	proteobacteria & Planctomycetales		distinct communities.		Transantarctic Mountains
Lake Bonney, McMurdo Dry Valleys	Hypersaline, meromictic, permanently ice-covered, lake separated into east and west lobes	18S libraries of watercolumn profile	Cryptophyta, Chlorophyta, Stramenopiles, Haptophyta, Choanoflagellida, Alveolate, Fungi & Ciliates	Photosynthesis	Population vertically stratified. Cryptophytes dominant in the shallow water and haptophytes in the mid-depths and chlorophytes in the deeper waters. Stramenopiles replaced haptophytes during polar night.	Bielewicz <i>et al.</i> , 2011	McMurdo Sound, Victoria Land & Transantarctic Mountains
Ekho, Organic and Deep Lakes, Vestfold Hills	Hypersaline. Ekho and Organic: meromictic and ice-covered ~9 months of the year Deep Lake: holomictic and never freezes	16S libraries of sediment	Organic: Cyanobacteria/chloroplasts, CFB, γ -proteobacteria, α -proteobacteria, Halobacteriales, Actinobacteria Ekho: Firmicutes, CFB, Cyanobacteria/chloroplasts, α -proteobacteria, γ -proteobacteria, Verrucomicrobiales, Spirochaetales. Deep: Halobacteriales & γ -proteobacteria	Heterotrophy	No phylotypes found in all samples. Distribution of bacterial classes similar between Ekho and Organic with <i>Roseovarius</i> common to both. <i>Marinobacter</i> and <i>Halomonas</i> common to Organic and Deep. Coverage: 86.5%, 90.8% and 96.6% for Ekho, Organic and Deep respectively.	Bowman <i>et al.</i> , 2000b	Pyrdz Bay, Vestfold & Larsemann Hills
Lake Vida, McMurdo Dry Valleys	Hypersaline, meromictic, permanently ice-covered	16S and 18S DGGE and 16S library of ice cover core	16S: Actinobacteria, CFB, γ -proteobacteria, Cyanobacteria. OD1, TM7 Firmicutes & Planctomycetales. 18S: Chlorophyta, fungi, Bacillariophyta, Apicomplexa, Cercozoa, Chrysophyceae, Chytridiomycota & Ciliophora.	Phototrophy, heterotrophy	Cell density highest at the surface. Phylogeny shows <i>Marinobacter</i> related to Lake Bonney isolate and bacterial sequences are similar to marine and polar organisms.	Mosier <i>et al.</i> , 2007	McMurdo Sound, Victoria Land & Transantarctic Mountains

Suribati Ike, Skarvsnes, Syowa Oasis	Hypersaline, meromictic sulfidic anoxic bottom waters.	16S libraries of water at the halocline	<i>Marinobacter</i> , <i>Halomonas</i> , <i>Pseudomonas</i> & <i>Halocella</i> .	Heterotrophy	<i>Marinobacter</i> isolates capable of DMSO-respiration were relatives of those detected in the lake water. Bacteria from the water column were unable to respire nitrate.	Matsuzaki <i>et al.</i> , 2006	Syowa Oasis
Clear, Pendant, Scale, Ace, Burton Lakes, Taynaya Bay, Vestfold Hills	Saline, meromictic lakes, high levels of accumulated sulphides (120 to >250mmol kg ⁻¹).	16S libraries of anoxic sediment	Bacteria: Firmicutes, Cyanobacteria/chloroplasts, CFB, δ -proteobacteria, α -proteobacteria, Planctomycetes, γ -proteobacteria, green non-sulfur bacteria, Chlamydiales, Verrucomicrobia & Actinobacteria. Eucarya: (2.5% of clones) Archaea: <i>Methanosarcina barkerii</i> or unknown Euryarchaeota group equidistant from Thermoplasma, Methanomicrobiales and Halobacteriales.	Sulphate reduction, methanogenesis, but also aerobic phototrophs and aerobic heterotrophy	Microbial diversity was surprisingly high. Lakes with similar physico-chemical and limnological traits had more similar microbial communities.	Bowman <i>et al.</i> , 2000a	Pyrdz Bay, Vestfold & Larsemann Hills
Lake Fryxell, McMurdo Dry Valleys	Brackish, meromictic permanently ice-covered.	<i>pufM</i> libraries, DGGE and RT-PCR of <i>pufM</i> transcripts in the water column.	α -proteobacteria & β -proteobacteria related to purple non-sulfur bacteria and aerobic anoxygenic phototrophs.	Anoxygenic photosynthesis.	Vertical stratification of the community down the water column. Purple and green sulfur bacteria not detected despite the high sulfide in the bottom waters. <i>pufM</i> transcripts only found below 9 m even though <i>pufM</i> genes are found throughout water column.	Karr <i>et al.</i> , 2003	McMurdo Sound, Victoria Land & Transantarctic Mountains

Lake Fryxell, McMurdo Dry Valleys	Brackish, meromictic permanently ice-covered.	16S and <i>dsrA</i> DGGE of water column	<i>Desulfovibrio</i> , <i>Desulfosarcina</i> , <i>Desulfobulbus</i> , and <i>Desulfobacter</i> groups.	Dissimilatory sulfate reduction	Phylogenetically diverse population of vertically stratified SRB.	Karr <i>et al.</i> , 2005	McMurdo Sound, Victoria Land & Transantarctic Mountains
Lake Fryxell, McMurdo Dry Valleys	Brackish, meromictic permanently ice-covered.	16S DGGE of water column	<i>Methanoculleus</i> , <i>Methanosarcina</i> , unclassified Euryarchaea, Methanosarcinales-group euryarchaea & marine benthic group C-like Crenarchaea	Hydrogenotrophic methanogenesis, potential anoxic methanotrophy	Diverse population of methanogenic Euryarchaea, unclassified Euryarchaea and divergent Crenarchaea detected in sediments and water column.	Karr <i>et al.</i> , 2006	McMurdo Sound, Victoria Land & Transantarctic Mountains
Nurume-Ike, Langhovde Hills, Syowa Oasis	Saline, meromictic	16S library of anoxic sediment	Archaea: Marine benthic group & unclassified Euryarchaeota. Bacteria: α -proteobacteria, δ -proteobacteria, Planctomycetes, Cyanobacteria/chloroplast, γ -proteobacteria, Actinobacteria, CFB, Verrucomicrobia & Spirochaetes.	Heterotrophy	Distribution of bacterial classes similar to lake sediment in the Vestfold Hills except α -proteobacteria relatively overrepresented and Firmicutes underrepresented.	Kurasawa <i>et al.</i> , 2010	Syowa Oasis
Heywood Lake and Shallow Bay, Signy Island	Heywood Lake: ice covered for ~9 months of the year, eutrophic due to organic inputs from seals, separated into two basins by shallow inlet. Shallow Bay: Coastal marine, ice-covered during winter	Archaeal 16S and universal 16S libraries of anoxic Sediment. Northern blots probed with methanogenic archaeal probes.	Heywood Lake blots: <i>Methanomicrobiales</i> , <i>Methanogenium</i> , <i>Methanosarcinales</i> & <i>Methanosaeta</i> . Shallow Bay blots: <i>Methanosarcinales</i> , <i>Methanomicrobiales</i> , & <i>Methanococcoides</i> . Heywood Lake archaea: <i>Methanosaeta</i> & <i>Methanogenium</i> . Shallow Bay archaea: <i>Methanogenium</i> , <i>Methanobolus</i> & <i>Methanococcoides</i> .	Acetoclastic & hydrogenotrophic methanogenesis, sulfur & metal oxidation, sulfate reduction.	Methanogenesis and sulfate reduction detected at both sites. Diversity of methanogenic archaea extremely low. Methanogenic archaea 34% and 0.2 % of community in Heywood Lake and Shallow Bay respectively. SRB 0.9% and 14.7% of community in Heywood Lake and Shallow Bay respectively.	Purdy <i>et al.</i> , 2003	Antarctic Peninsula

			<p>Heywood Lake SRB: <i>Desulfovibrio</i>, <i>Desulfotalea/Desulforhopalus</i>, <i>Desulfobulbus</i> & <i>Desulfobacteriaceae</i>.</p> <p>Shallow Bay SRB: <i>Desulfotalea/Desulforhopalus</i>, <i>Desulfobacterium</i>, <i>Desulfobulbus</i> & <i>Desulfobacteriaceae</i>.</p>				
Sombre Lake, Signy Island	Freshwater, ice-covered for ~9 months of the year, oligotrophic (N and P) limited.	16S libraries, DGGE, 16S libraries and FAME analysis of isolates and FISH of water column profile	<p>16Sofisolates: β-proteobacteria, Firmicutes, Actinobacteria, α-proteobacteria & γ-proteobacteria</p> <p>FAME: Firmicutes, Actinobacteria, γ-proteobacteria, β-proteobacteria & α-proteobacteria</p> <p>Clones: Actinobacteria, CFB, β-proteobacteria, α-proteobacteria, Spirochaetales, δ-proteobacteria, γ-proteobacteria & Verrucomicrobia</p> <p>FISH: β-proteobacteria, CFB, α-proteobacteria & γ-proteobacteria.</p> <p>DGGE: Actinobacteria, CFB & β-proteobacteria</p>	Heterotrophic, mainly respiratory metabolisms	<p>Relative abundances shown by clone libraries and FISH the same.</p> <p>Few genera were found by culture-dependent and independent techniques.</p> <p>16S isolate library and 16S clone library were significantly different. 16S clone library covers the largest spread of phyla but is missing Firmicutes.</p> <p>Overall β-proteobacteria were dominant.</p>	Pearce <i>et al.</i> , 2003a	Antarctic Peninsula
Moss Lake, Signy Island	Freshwater, ice-covered for ~9 months of the year, oligotrophic (N and P) limited.	16S DGGE and FISH of water column profile	<p>β-proteobacteria, CFB, α-proteobacteria, γ-proteobacteria, Actinobacteria & Cyanobacteria.</p> <p>< 1% of cells hybridized with Archaeal FISH probe.</p>	Heterotrophy, mainly respiratory metabolisms, phototrophy	<p>Very little vertical stratification of population.</p> <p>16S sequences similar to temperate and cold aquatic systems.</p>	Pearce <i>et al.</i> , 2003b	Antarctic Peninsula
Moss, Sombre and Heywood Lakes, Signy Island	Freshwater, ice-covered for ~9 months of the year, oligotrophic to	16S DGGE of water column profile over	Not determined	Not determined	Lakes were physically and chemically stratified in winter and mixed in summer. Variation in	Pearce, 2005a	Antarctic Peninsula

	eutrophic status.	the winter to summer transition			bacterial community structure correlated with lake chemistry. Bacterial community still unstable during holomixis.		
Heywood Lake, Signy Island	Freshwater, ice-covered for ~9 months of the year, eutrophic due to organic inputs from seals, separated into two basins by shallow inlet.	16S libraries, DGGE, 16S libraries and FAME analysis of isolates and FISH of water column profile	<p>16Sclones: β-proteobacteria, α-proteobacteria, & Actinobacteria.</p> <p>FAME: Actinobacteria, Firmicutes, γ-proteobacteria & α-proteobacteria.</p> <p>FISH: β-proteobacteria, CFB, γ-proteobacteria & α-proteobacteria.</p> <p>DGGE: Actinobacteria, CFB, Gram-positives & β-proteobacteria.</p>	Heterotrophy, mainly respiratory metabolisms, phototrophy	<p>Clone library coverage 71.7%.</p> <p>Similar genera to Moss and Sombre Lakes.</p> <p>Actinobacteria and marine α-proteobacteria enriched compared to oligotrophic lakes while Cyanobacteria underrepresented.</p> <p>Species evenness is higher than Sombre or Moss Lakes.</p>	Pearce <i>et al.</i> , 2005b	Antarctic Peninsula
Lakes Boeckella, Esperanza, Flora, Encantado, Chico and Pingüi, Hope Bay, Antarctic Peninsula and Lakes L, M, W and Z, King George Island	Freshwater, oligotrophic except Pingüi and Boeckella which were eutrophic and mesotrophic respectively.	18S DGGE of surface water (20—3 μ m)	Chrysophyta, Chlorophyta, Dictyochophyceae, Bacillariophyceae & Cerozoa.	photosynthesis	<p>Molecular surveys showed greater level of diversity exists than can be determined by light microscopy.</p> <p>Lake communities varied depending on trophic status.</p> <p>Lakes in both regions shared bands belonging to Chrysophyta although they were 220 km apart.</p>	Unrein <i>et al.</i> , 2005	Antarctic Peninsula

					Dictyochophyceae and Cercozoa restricted to oligotrophic lakes.		
Lakes Boeckella, Esperanza, Flora, Encantado, Chico and Pingüi, Hope Bay, Antarctic Peninsula and Lakes W and Z, King George Island	Freshwater, oligotrophic except Pingüi and Boeckella which were eutrophic and mesotrophic respectively.	16S DGGE of surface water (3—0.2 µm)	CFB, Actinobacteria, β-proteobacteria & Cyanobacteria.	Heterotrophy, photosynthesis	<p>Cluster analysis showed Lake communities from the Hope Bay formed one group while Lakes Chico, Pingüi and Boeckella formed another subgroup with King George Island lakes.</p> <p>63.7% of variance is explained by axis 1 and 2 of Canonical Correspondence Analysis (40.4% phosphate, dissolved inorganic nitrogen and pH; 23.3% dissolved inorganic nitrogen).</p> <p>Temporal variation is not as pronounced as differences due to trophic status.</p>	Schiaffino <i>et al.</i> , 2009	Antarctic Peninsula
Lakes Limnopolar, Midge, Chester, Chica, Turbio, Somero & Refugio, Livingston Island.	Fresh to saline, all oligotrophic except for Refugio which was eutrophic.	16S DGGE of from surface water	CFB & α-proteobacteria	Heterotrophy, phototrophy	<p>Cluster analysis showed deep lakes of the plateau grouped together while Somero and Refugio were separate groups.</p> <p>Over 90% of variance was explained by chemical parameters related to trophic status and salinity.</p>	Villaescusa <i>et al.</i> , 2010	Antarctic Peninsula

Lake Vostok	Largest subglacial lake, isolated from surface 420, 000 years	16S library of accretion ice core from 3590 m	α -proteobacteria, β -proteobacteria, & Actinomycetes	Potential heterotrophy	No Archaea were amplified using Archaeal primers. No biological incorporation of selected substrates.	Priscu <i>et al.</i> , 1999	Lake Vostok
Lake Vostok	Largest subglacial lake, isolated from surface 420, 000 years	16S library of accretion ice core from 3590 and 3603 m and isolation of bacteria	α -proteobacteria, β -proteobacteria, Firmicutes, Actinobacteria & CFB	Potential heterotrophy	Bacteria appear related to isolates from similarly cold environments. No archaea were amplified using archaeal primers.	Christner <i>et al.</i> , 2001	Lake Vostok
Lake Vostok	Largest subglacial lake, isolated from surface 420, 000 years	16S, <i>cbbL/rbcL</i> and <i>hoxV-hupL</i> library of accretion ice core from 3561 m	<i>Hydrogenophilus thermoluteolus</i>	Potential hydrogenotrophy	Thermophilic chemolithoautotrophic <i>Hydrogenophilus thermoluteolus</i> 16S rRNA, RubisCO and NiFe-Hydrogenase genes detected.	Lavir <i>et al.</i> , 2006	Lake Vostok
Lake Vostok	Largest subglacial lake, isolated from surface 420, 000	16S library of Vostok drilling fluid recovered from 4 depths of the bore hole.	<i>Sphingomonas</i> , potential contaminants related to human/animal pathogens or saprophytes and environmental contaminants.	Hydrocarbon degrading heterotrophs	New contaminant bacteria identified that were associated with hydrocarbon-based drilling fluid.	Alekhina <i>et al.</i> , 2007	Lake Vostok

16S, 16S rRNA gene sequencing; 18S, 18S rRNA gene sequencing, DGGE, Denaturing gradient gel electrophoresis; CFB-group, Cytophaga/Flavobacteria/Bacteroidetes, SRB, sulfate-reducing bacteria.